



1600

#10

## RAW SEQUENCE LISTING

DATE: 02/24/2003

PATENT APPLICATION: US/09/928,522A

TIME: 15:20:06

Input Set : A:\Pm8808a.app

Output Set: N:\CRF4\02242003\I928522A.raw

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3 <110> APPLICANT: SPURLOCK, MICHAEL E.
5 <120> TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, ANTISENSE AND ANTIBODY
7 <130> FILE REFERENCE: PM-8808-A
9 <140> CURRENT APPLICATION NUMBER: 09/928,522A
10 <141> CURRENT FILING DATE: 2001-08-13
12 <150> PRIOR APPLICATION NUMBER: 08/688,908
13 <151> PRIOR FILING DATE: 1996-07-31
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 36
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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34 <213> ORGANISM: Artificial Sequence
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46 <213> ORGANISM: Bovine sp.
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (6)..(443)
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54 Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
55 1 5 10 15
57 aca att gtc acc agg atc aat gac atc tca cac acg cag tcc gtc tcc 98
58 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
59 20 25 30
61 tcc aaa cag agg gtc act ggt ttg gac ttc atc cct ggg ctc cac cct 146
62 Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
63 35 40 45
65 ctc ctg agt ttg tcc aag atg gac cag aca ttg gcg atc tac caa cag 194

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66 Leu Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln
67      50      55      60
69 atc ctc acc agt ctg cct tcc aga aat gtg gtc caa ata tcc aat gac 242
70 Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn Asp
71      65      70      75
73 ctg gag aac ctc cgg gac ctt ctc cac ctg ctg gcc gcc tcc aag agc 290
74 Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys Ser
75 80      85      90      95
77 tgc ccc ttg ccg cag gtc agg gcc ctg gag agc ttg gag agc ttg ggt 338
78 Cys Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu Gly
79      100      105      110
81 gtc gtc ctg gaa gcc tcc ctc tac tcc acc gag gtg gtg gcc ctg agc 386
82 Val Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
83      115      120      125
85 cgg ctg cag ggg tca cta cag gac atg ttg cgg cag ctg gac ctc agc 434
86 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu Ser
87      130      135      140
89 cct gaa tgc agcgct 449
90 Pro Glu Cys
91      145
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95 <211> LENGTH: 146
96 <212> TYPE: PRT
97 <213> ORGANISM: Bovine sp.
99 <400> SEQUENCE: 4
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101 1      5      10      15
103 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
104      20      25      30
106 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Leu
107      35      40      45
109 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile
110      50      55      60
112 Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn Asp Leu
113 65      70      75      80
115 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys Ser Cys
116      85      90      95
118 Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu Gly Val
119      100      105      110
121 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
122      115      120      125
124 Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro
125      130      135      140
127 Glu Cys
128 145
131 <210> SEQ ID NO: 5
132 <211> LENGTH: 445
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens

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139 tggacttcat tcctgggctc caccatcc tgaccttacc caagatggac cagacactgg 180
140 cagtctacca acagatcctc accagtatgc cttccagaaa cgtgatccaa atatccaacg 240
141 acctggagaa cctccgggat cttcttcacg tgctggcctt ctctaagagc tgccacttgc 300
142 cctggggccag tggcctggag accttggaac gcctgggggg tgctcctggaa gcttcaggct 360
143 actccacaga ggtggtggcc ctgagcaggc tgcaggggtc tctgcaggac atgctgtggc 420
144 agctggacct cagccctggg tgctg                                     445
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148 <211> LENGTH: 86
149 <212> TYPE: DNA
150 <213> ORGANISM: Murine sp.
152 <400> SEQUENCE: 6
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154 ccaggatcaa tgacatttca cacacg                                     86
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158 <211> LENGTH: 167
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
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166 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
167 20 25 30
169 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
170 35 40 45
172 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
173 50 55 60
175 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
176 65 70 75 80
178 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
179 85 90 95
181 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
182 100 105 110
184 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
185 115 120 125
187 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
188 130 135 140
190 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
191 145 150 155 160
193 Leu Asp Leu Ser Pro Gly Cys
194 165
197 <210> SEQ ID NO: 8
198 <211> LENGTH: 167
199 <212> TYPE: PRT
200 <213> ORGANISM: Murine sp.
202 <400> SEQUENCE: 8
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204      1              5              10              15
206 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
207              20              25              30
209 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
210              35              40              45
212 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
213              50              55              60
215 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
216      65              70              75              80
218 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
219              85              90              95
221 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
222              100              105              110
224 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
225              115              120              125
227 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
228              130              135              140
230 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
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239 <212> TYPE: DNA
240 <213> ORGANISM: Murine sp.
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244 attctgagtt tgtccaagat ggaccagact ctggcagtct atcaacaggt cctcaccagc 120
245 ctgccttccc aaaatgtgct gcagatagcc aatgacctgg agaatctccg agacctctc 180
246 catctgctgg ccttctccaa gagctgctcc ctgcctcaga ccagtggcct gcagaagcca 240
247 gagagcctgg atggcgctct ggaagcctca ctctactcca cagaggtggt ggctttgagc 300
248 aggctgcagg gctctctgca ggacattctt caacagttgg atgttagccc tgaatgctg 359

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/928,522A

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